

**IN THE CLAIMS:**

1. (Original) A nucleic acid information detection method wherein a target nucleic acid and probes made solid phase on a carrier and having a complementary sequence with at least a portion of said target nucleic acid sequence are contacted with each other in order to form hybrids between said target nucleic acid and said probes, and the amount of signal generated depending on the amount of hybrids is measured in order to detect the information on the target nucleic acid,

said method including kinetically obtaining data of said signal.

2. (Original) A nucleic acid information detection method according to claim 1, wherein obtaining the data of said signal is performed while changing a measurement condition or a detection condition of a reaction.

3. (Original) A nucleic acid information detection method according to claim 2, wherein obtaining the data of said signal is performed while changing at least one of; a reaction temperature, a composition, a volume, and a type of reaction solution.

4. (Original) A nucleic acid information detection method according to claim 3, wherein said change is for the reaction temperature.

5. (Original) A nucleic acid information detection method wherein a perfect matched probe having a perfect complementary sequence with respect to at least part of a target nucleic acid sequence, and one or more types of imperfectly matched probes having at least one part of the perfect matched probe mutated are contacted with said target nucleic acid in order to form hybrids between said target nucleic acid, and said perfect matched probe or

said imperfect matched probes, so that the information on the target nucleic acid can be detected based on a difference in binding strength of the hybrids,

said method including kinetically obtaining data of said signal while changing continuously or stepwise the condition for measuring or detecting the signal from said hybrids.

6. (Original) A nucleic acid information detection method according to claim 5, wherein obtaining the data of said signal is performed while changing at least one of; a reaction temperature, a composition, a volume, and a type of reaction solution.

7. (Original) A nucleic acid information detection method according to claim 6, wherein said change is for the reaction temperature

8. (Original) A nucleic acid information detection method according to claim 7, wherein said change of the reaction temperature is to increase the temperature from a temperature lower than a  $T_m$  value of the hybrids to be detected to a temperature higher than the  $T_m$  value.

9. (Original) A nucleic acid information detection method according to claim 7, wherein said change of the reaction temperature is a temperature cycle of one or more times comprising increase and decrease between a temperature lower than the  $T_m$  value to a temperature higher than the  $T_m$  value.

10. (Currently Amended) A nucleic acid information detection method according to ~~either claim 8 or claim 9~~, including a step of measuring a maximum value of the signal strength while increasing said temperature.

11. (Currently Amended) A nucleic acid information detection method according to ~~either claim 8 or claim 9~~, including a step of measuring an amount of change in the signal strength while increasing said temperature.

12. (Original) A nucleic acid information detection method according to any one of claim 5 through claim 11, further comprising the steps of continuously or stepwise increasing the temperature at which a signal from said hybrid is measured, measuring the change in the signal strength from said hybrid between respective temperatures, and maintaining the temperature when the amount of change starts to decrease.

13. (Currently Amended) A nucleic acid information detection method according to any one of claim 1 through claim ~~12~~ 11, wherein in an identical system where identical reaction conditions are applicable, a plurality of types of probes are used in order to detect the information on a plurality of types of nucleic acids at the same time.

14. (Currently Amended) A nucleic acid information detection method according to any one of claim 1 through claim ~~13~~ 11, wherein said probes are a plurality of types of probes having a plurality of types of sequences and said probes have mutually overlapped sequences.

15. (Currently Amended) A nucleic acid information detection method according to any one of claim 1 through claim ~~14~~ 11, wherein said probes having a plurality of types of sequences comprise overlapping probes of; a perfect matched probe having a perfect complementary sequence at least partially with said target nucleic acid sequence, one or more types of imperfect matched probes having at least one partial mutation in said perfect

matched probe, and said perfect matched probe and said imperfect matched probe having an extended or shortened base sequence on both ends or one end.

16. (Currently Amended) A nucleic acid information detection method according to any one of claim 1 through claim ~~15~~ 11, further comprising a step of comparing an analysis result of a probe group having a lower T<sub>m</sub> value among the overlapping probes with an analysis result of a probe group having a higher T<sub>m</sub> value, thereby deciding the nucleic acid information.

17. (Currently Amended) A nucleic acid information detection method according to any one of claim 1 through claim ~~16~~ 11, wherein the probes have sequences (SEQ ID NO: 59 to 69) comprising 20mer base sequences for analyzing K-ras codon12.

18. (Currently Amended) A nucleic acid information detection method according to any one of claim 1 through claim ~~17~~ 11, wherein the probes have sequences (SEQ ID NO: 70 to 83) comprising 17mer base sequences for analyzing K-ras codon12.

19. (Currently Amended) A nucleic acid information detection method according to any one of claim 1 through claim ~~18~~ 11, wherein the probes consist of probes having sequences of (SEQ ID NO: 56 to 83 ~~69~~) ~~17mer~~ 20mer base sequences for analyzing K-ras codon12, and probes having sequences of (SEQ ID NO: 70 to 83) ~~20mer~~ 17mer base sequences for analyzing K-ras codon12.

20. (Currently Amended) A nucleic acid information detection method according to any one of claim 1 through claim 19 11, wherein said hybrid formation is

performed by making a liquid sample including a target nucleic acid contact with a probe fixed onto a porous body.

21. (Original) A nucleic acid information detection method according to claim 20, further comprising a step of making said liquid sample reciprocate once or a plurality of times in said porous body.

22. (Currently Amended) A nucleic acid information detection method according to any one of claim 1 through claim ~~21~~ 11, wherein said signal is detected based on detection of a fluorescent marker.

23. (Currently Amended) A nucleic acid information detection method according to any one of claim 1 through claim ~~22~~ 11, wherein said target nucleic acid is any one of an oncogene, an intracellular drug resistance gene, a cell cycle regulator gene, and an apoptosis related gene, or a combination of these.

24. (Original) A nucleic acid information detection apparatus comprising: a sample storage container for containing a sample including a target nucleic acid; a nucleic acid reaction carrier including a porous structure which can fix said nucleic acid and connected to said container; a driving device for mobilizing said sample under control, between said container and said nucleic acid reaction carrier without leaking; a temperature control device for controlling a reaction temperature on said reaction carrier; and a device for detecting a signal from a hybrid between a target nucleic acid and probes formed on said porous structure.

25. (Original) A nucleic acid information detection apparatus according to claim 24, further comprising: one or more solution storage containers for storing solutions connected to said nucleic acid reaction carrier and to contain types of solutions different to the sample solution including the target nucleic acid; and a device which appropriately mixes the various solutions contained in said solution storage containers and sends these to said nucleic acid reaction carrier.

26. (Original) A nucleic acid information detection apparatus according to either one of claim 24 and claim 25, wherein said target nucleic acid is any one of an oncogene, an intracellular drug resistance gene, a cell cycle regulator gene, and a apoptosis related gene, or a combination of these.

27. (New) A nucleic acid information detection method according to claim 9, including a step of measuring a maximum value of the signal strength while increasing said temperature.

28. (New) A nucleic acid information detection method according to claim 9, including a step of measuring an amount of change in the signal strength while increasing said temperature.

29. (New) A nucleic acid information detection method according to claim 27 or 28, further comprising the steps of continuously or stepwise increasing the temperature at which a signal from said hybrid is measured, measuring the change in the signal strength from said hybrid between respective temperatures, and maintaining the temperature when the amount of change starts to decrease.

30. (New) A nucleic acid information detection method according to claim 27 or 28, wherein in an identical system where identical reaction conditions are applicable, a plurality of types of probes are used in order to detect the information on a plurality of types of nucleic acids at the same time.

31. (New) A nucleic acid information detection method according to claim 27 or 28, wherein said probes are a plurality of types of probes having a plurality of types of sequences and said probes have mutually overlapped sequences.

32. (New) A nucleic acid information detection method according to claim 27 or 28, wherein said probes having a plurality of types of sequences comprise overlapping probes of; a perfect matched probe having a perfect complementary sequence at least partially with said target nucleic acid sequence, one or more types of imperfect matched probes having at least one partial mutation in said perfect matched probe, and said perfect matched probe and said imperfect matched probe having an extended or shortened base sequence on both ends or one end.

33. (New) A nucleic acid information detection method according to claim 27 or 28, further comprising a step of comparing an analysis result of a probe group having a lower  $T_m$  value among the overlapping probes with an analysis result of a probe group having a higher  $T_m$  value, thereby deciding the nucleic acid information.

34. (New) A nucleic acid information detection method according to claim 27 or 28, wherein the probes have sequences (SEQ ID NO: 59 to 69) comprising 20mer base sequences for analyzing K-ras codon12.

35. (New) A nucleic acid information detection method according to claim 27 or 28, wherein the probes have sequences (SEQ ID NO: 70 to 83) comprising 17mer base sequences for analyzing K-ras codon12.

36. (New) A nucleic acid information detection method according to claim 27 or 28, wherein the probes consist of probes having sequences of (SEQ ID NO: 56 to 69) 20mer base sequences for analyzing K-ras codon12, and probes having sequences of (SEQ ID NO: 70 to 83) 17mer base sequences for analyzing K-ras codon12.

37. (New) A nucleic acid information detection method according to claim 27 or 28, wherein said hybrid formation is performed by making a liquid sample including a target nucleic acid contact with a probe fixed onto a porous body.

38. (New) A nucleic acid information detection method according to claim 37, further comprising a step of making said liquid sample reciprocate once or a plurality of times in said porous body.

39. (New) A nucleic acid information detection method according to claim 27 or 28, wherein said signal is detected based on detection of a fluorescent marker.

40. (New) A nucleic acid information detection method according to claim 27 or 28, wherein said target nucleic acid is any one of an oncogene, an intracellular drug resistance gene, a cell cycle regulator gene, and an apoptosis related gene, or a combination of these.